

Figure 1(a)

accession # Q55957

```

HHV8PEP      -----MTPRSR-LATLGTVILLVCFCAG--AAHSRGDTFQ--
RHESRHADPEP -----MMITNRTRRLRAWVVIIGTAVG--ENVTTPKGAT--
MURH68PEP    -----MYPTVKSMRVAHLTNLLTLLCLLCHTHLYVCQPTTLR--
BOVINEH4PEP  YYKTILFFALIKVCSFNQTTTHSTTTTSPSISSTTSSTTTSTSKPSNTTSTNSSLAAS PQ
ATELINEH3PEP -----MTLNR---CVLLIVLTFSTACS-----Q--
SAIMIRIPEP   -----MVPNK---HLLLIILSFSTACG-----Q--
EQH2PEP      -----MGVGGGPRVVLCLWCVAALLCQGVAEVVAETTTTFFA--
EQH5PEP      -----MVAWFGWLWGFARLMATLALLCGRVALDESSATPSIPP--
ALCELPEP     -----MAHTGSTVCAFLIFAVLKNVFCQPTPTSSEVEDVIPEAN-
EBVPEP       -----MTRRRVLSVVVLLAALACRLGA-----Q--TPEQ--

HHV8PEP      --TSSSPTPPGSSSKAPTKPGEEASGPKSVDFYQFRVCSAS-ITGELFRFNLEQTCPTDK
RHESRHADPEP  --TTAKPTP-GPS--TPTPP---ENPPR-AEAFKFRVCSAS-ATGELFRFNLEKTCPGTE
MURH68PEP    --QPSDMTP-AQDAPTETPPPLSTNTNR--GFEYFRVCGVA-ATGETFRFDLDKTCPTQ
BOVINEH4PEP  NTSTSKPSTDNQGTSTPTIPTVDDTAS-KNFYKRVCSASSSSGELFRFDLDQTCPTDK
ATELINEH3PEP ----TTPASSDEN--GKTPAIEK--EYF----K-YRVCSAS-TTGELFRFNLDRACPSTE
SAIMIRIPEP   ----TPTTAVEK--NKTQAIYQ--EYF----K-YRVCSAS-TTGELFRFDLDRTCPSTE
EQH2PEP      ---THRPEVVAEE--NPANP-----FLP----F--RVCGASPTGGEIFRFPLEESCNPTE
EQH5PEP      ---THKPAVHHED--NTTNP-----FLL----F--RVCGASPTG-EIFRFPLEENCNPTE
ALCELPEP     --TVSDNIIRQOR--NNTAKGIHSDPSA----FPFRVCSAS-NIGDIFRQTSHSNCPNTK
EBVPEP       ---PAPPATTVQP--TATRQ-----QTS----FPFRVCELS-SHGDLFRFSSDIQCPSPFG

HHV8PEP      DKY-HQEGILLVYKKNIVPHIFKVRRYRKIATSVTVYRGLTES--AITNKYELPRVPPLY
RHESRHADPEP  DKT-HQEGILMVFKKNIVPHIFKVRRYRKVATSVTVYRGWTET--AVTGKQEVIRPVPQY
MURH68PEP    DKK-HVEGILLVYKINIVPYIFKIRRYRKIITQLTIWRGLTTS--SVTGKFEMATQAHEW
BOVINEH4PEP  DKK-HVEGILLVLKKNIVPYIFKVRKYRKIATSVTVYRGWSQA--AVTNRDDISRAIPYN
ATELINEH3PEP DKV-HREGILLVYKKNIVPHIFKVRYYKKIATSVRIFNGWSREGVAITNKWELSRAPVKY
SAIMIRIPEP   DKV-HKEGILLVYKKNIVPYIFKVRYYKKITTSVRIFNGWTREGVAITNKWELSRAPVKY
EQH2PEP      DKD-HIEGIALIYKTNIVPYVFNVRKYRKIMTSTTIYKGWSED--AITNQHTRSYAVPLY
EQH5PEP      DKE-HVEGILLIYKTNIVPYIFNVRKYRKLVSTTIYKGWSQD--AITNQYTSFAMPLW
ALCELPEP     DKE-HNEGILLIFKENIVPYVFKVRKYRKIVTTSTIYNGIYAD--AVTNQHVFSKSVPIY
EBVPEP       TRENHTEGLLMVFKDNIIPYSFKVRSYTKIVTNILIYNGWYAD--SVTNRHEEKFSVDSY

HHV8PEP      EISHMDSTYQCFSSMKVNVNGVENTFTDRDDVNTTVFLQPVEGLTDNIQRYFSQPVIYAE
RHESRHADPEP  EINHMDTTYQCFSSMRVNVNGIVNTYTDRDFTNQTVFLQPVEGLTDNIQRYFSQPVLYTT
MURH68PEP    EVGDFDSIYQCYNSATMVVNNVRQVYVDRDGVNKTVNIRPVDGLTGNIQRYFSQPTLYSE
BOVINEH4PEP  EISMIDRTYHCFSAMATVINGILNTYIDRDSSENKSVPLQPVAGLTENINRYFSQPLIYAE
ATELINEH3PEP EINLMDKNYQCHNCMQIEVNGLLNSYCDRDGNNKTVDLKPVDGLTGAITRYVSQPKIFAD
SAIMIRIPEP   EIDIMDKTYQCHNCMQIEVNGMLNSYDRDGNNKTVDLKPVDGLTGAITRYISQPKVFAD
EQH2PEP      EVQMMDHYYQCFSAVQVNEGGHVNTYVDRDGNWETAFLKPADGLTSSITRYQSQPEVYAT
EQH5PEP      EARLVDYNYECYNGIQVTENGHLTTYVDRDGYNESVRLVPADGLTSSIRRYHSQPELYVT
ALCELPEP     ETRRMDTIYQCYNSLDVTVGGNLLVYTDNDGSNMTVDLQPDGLSNSVRRYHSQPEIHAE
EBVPEP       ETDQMDTIYQCYNAVKMTKDGLTRVYVDRDGVNITVNLKPTGGLANGVRRYASQTELYDA

HHV8PEP      PGWFPGIYRVRTTVNCEIVDMIARSAEPYNYFVTSLGDTVEVSPFCYNSSCST-TPSNK
RHESRHADPEP  PGWFPGIYRVRTTVNCEIVDMIARSAEPYSYFVTALGDTVEVSPFCHNDSTCSV-AEKTE
MURH68PEP    PGWMPGFYRVRTTVNCEIVDMVARSMYPNYIATALGDSLELSPFQTFDNTS QS-TAPKR
BOVINEH4PEP  PGWFPGIYRVRTTVNCEIVDMYARSVEPYTHFITALGDTIEISPFCHNNSQCTTGNSTSR
ATELINEH3PEP AGWLWGTYKTRRTTVNCEIVEMFARSADPYTYFVTALGDTVEVSPFCDAENSCPN----AS
SAIMIRIPEP   PGWLWGTYRTRRTTVNCEIVDMFARSADPYTYFVTALGDTVEVSPFCVDVNSCPN----AT
EQH2PEP      PRNLLWSYTTRTTVNCEIVTEMSARSMKPFYFVTASGDTIEMSPFLKENGTEPE--KILK
EQH5PEP      PRNLLWSYTTRTTVNCEIVDMTARSHKPFYFVTASGDSIETSPFYT-NASR-----R
ALCELPEP     PGWLLGGYRRRTTVNCEIVTETDARAVPPFRYFITNIGDTIEMSPFWSKAWNETEFS--GE
EBVPEP       PGWLIWYRTRRTTVNCEITDMAKSNSPFDFFVTGQTVEMSPFYDGKNKETF----HE

```

Figure 1(b)

20250404 095500T

HHV8PEP
RHEsrHADPEP
MURH68PEP
BOVINEH4PEP
ATELINEH3PEP
SAIMIRIPEP
EQH2PEP
EQH5PEP
ALCELPEP
EBVPEP

HHV8PEP
RHEsrHADPEP
MURH68PEP
BOVINEH4PEP
ATELINEH3PEP
SAIMIRIPEP
EQH2PEP
EQH5PEP
ALCELPEP
EBVPEP

HHV8PEP
RHEsrHADPEP
MURH68PEP
BOVINEH4PEP
ATELINEH3PEP
SAIMIRIPEP
EQH2PEP
EQH5PEP
ALCELPEP
EBVPEP

HHV8PEP
RHEsrHADPEP
MURH68PEP
BOVINEH4PEP
ATELINEH3PEP
SAIMIRIPEP
EQH2PEP
EQH5PEP
ALCELPEP
EBVPEP

HHV8PEP
RHEsrHADPEP
MURH68PEP
BOVINEH4PEP
ATELINEH3PEP
SAIMIRIPEP
EQH2PEP
EQH5PEP
ALCELPEP
EBVPEP

NGLSVQVVLNHTVVITYSDRGTSPTPQNRIFVETGAYTLWSASESKTTAVCPALALWKTFFPR
NGLGARVLNTYTMVDFATR--APTETRVFADSGEYTVSWKAEDPKSAVCALTLWKTFFPR
ADMVRREVKNYKFVDYNNRGTAPOQSRTFLETSPATYSWKTATRTQATCDLVHWKTFFPR
DATKVVIEENHQTVDYERRG-HPTKDKRIFLKDEEYTLISWKAEDRERAICDFVIWKTFFPR
DVLSSQVDFNHTVVVDYGNRATSQQHKGKRIFAHTLDYSVSWEAINKTTSVCSMVFWKGFQR
DVLVSQIDLNHTVVVDYGNRATSQQHKKRIFAHTLDYSVSWEAVNKSASVCSMVFWKSFQR
RPHSIQLLKNYAVTKYGVGLGQADNATRFPAIFGDYSLSWKATTENSZYCDLILWKGFNS
VP--VQVLYNYSVTYDYGVLGSGENVTRFFATLNDFSISWKAATENSZYCPLVLWKGFPS
PDRTLTVAKDYRVVDYKFRGTQPOGHTRIFVDKEEYTLWSAQQFRNISYCRWAHWKSFND
RADSFHVRTNYKIVDYDNRGTNPQGERRAFLDKGTYTLWSKLENR-TAYCPLQHWQTFDS

SIQTTTHEDSFHFVANEITATFTAP---LTPVANFTDTYSCLTSDINTTLNASKAKLASTH
AIQTTHEASYHFVANDVTATFTSP---LSEVANFTGTYSCLDEVIQKTLNDTIKKLSDTH
AIQTAHEHSYHFVANEVTATFTNP---LTEVENFTSTYSCVSDQINKTISEYIQLNNSY
AIQTIHNESFHFVANEVTASFLTSNQEETELRGNTEILNCMNSTINETLEETVKKFNKSH
AIQTEHDSTYHFIANEITAGFSTS---KETLASFSSEYSCLMDSINSTLTDKIGRVNNTH
AIQTEHDLTYHFIANEITAGFSTV---KEPLANFTSDYNCLMTHINTTLEDKIARVNNTH
AIQTQHNSSLHFIANDITASFSTP---LEEEAN-FNETFKCIWNNTQEEIQQKLEVEKTH
AIQTKHEKSYHFIAADAVTASFTTP---LTDETSYFNNTTYQCAWQDIEGEIQRFPDPSKTH
AIKTEHGKSLHFVANDITASFYTP---NTQTREVLGKHVCLNNTIESELKSLAKVNDTH
TIATETGKSIHFVTDEGTSSFVTN---TTVGIELPDAFKCIEEQVNKTMHEKEYEAVQDRY

VP-NGTVQYFHTTGGLYLWVQPMASAINLTHAQ-GDSGNPTSSPPPSASP-----M
VT-NGSAQYKTEGGLFLLWQPLTPLSLVDEMRLNG---TTPAP---P-----A
VA-SGKTQYFKTDGNLYLIWQPLEHPEIEDID--EDSDPEPTAP---P-----K
IR-DGEVKYKFTNGGLFLIWAQMKPLNLSEHT-----N-YTIER---N-----N
VP-NGTAQYFKTEGGMILWVQPLTAIELEEAMIEATTVSPTPLS-----T
TP-NGTAEYYQTEGGMILWVQPLIAIELEEAMLEATTSPVTPSAP-----T
RP-NGTAKVYKTTGNLYIYVQPLIQIDLLDTHAKLYNLTNATASPTSTP-----T
AR-NGSVQIYKTSNLYVWQPLVQDLDDLAHAKTINSTDNSTSPPTAPN-----TT
SP-NGTAQYLYLTNGGLLLWVQPLVQQLLDAKGLLDVAVKKQNTTTT-----T
TKGQEAITYFITSGGLLLAWLPLTPRSLATVKNLTELTTPTSSPPSSPSPAPSAARGST

TTSASRRKRRSASTAAAGG---GGSTDN-----LSYTQLOQFAYDKLRDGINQVLEELSRA
TTSTVSRVRRSVNTNEQ-----ATDN-----LAAPQLOQFAYDKLRASINKVLEELSRA
STRRKREAADNGNSTSEVS---KGSNP-----LITAQIQFAYDKLTTSVNNVLEELSRA
KTGNKSRQKRSVDTKTFQG-----AKG-----LSTAQVQYAYDHLRTSMNHILEELTKT
AHLTSRRTGRRKRDVSAG-----SENS-----VLLAQIQYAYDKLRQSINNVEELAIT
SSSRSKRAIRSIRDVSAG-----SENN-----VFLSQIQYAYDKLRQSINNVEELAIT
-TTSPPRRRRRTSSVSGGG---NNGDNSTKEESVAASQVQFAYDNLRSINRVLGELSRA
TSTSSRRKRRDTGNTATNN---SSSNNSSMEENLATSQVQFAYDQLRKSINRVLEQLSRV
TTTRSRRQRRSVSSGIDDV---YTAEST-----ILLTQIQFAYDTLRAQINNVEELSRA
PAAVLRRRRRDAGNATTPVPPTAPGKSLGTLNPNPATVQIQFAYDSLRRQINRMLGDLARA

WCREQVRDNLMWYELSKINPTSVMTAIYGRPVSAKFVGDAISVTECINVDQSSVNIHKS
WCREQVRDTYMWYELSKINPTSVMTAIYGRPVSAKFVGDAISVTDCAVDQASVSIHKS
WCREQVRDTLMWYELSKVNPTSVMSAIYGKPVAAARYVGDAISVTDCAVDQSSVNIHQSL
WCREQKDNLMWYELSKINPTSVMSAIYGKPVAVKAMGDVAFMVSECINVDQASVNIHKS
WCREQVRQTMWYELIAKINPTSVMTAIYGKPVSAKALGDVISVTECINVDQSSVSIHKS
WCREQVRQTMWYELIAKINPTSVMTAIYGKPVSRKALGDVISVTECINVDQSSVSIHKS
WCREQYRASLMWYELSKINPTSVMSAIYGRPVSAKLIGDVVSVDICISVDQKSVFVHKNM
WCQNQYRASLMWYELSKINPTSVMSAIYGRPVSAKLIGDVVSVDICISVDQKSVFVHRNL
WCREQHRASLMWNEELSKINPTSVMSIYGRPVSAKRIGDVISVSHCVVDQDSVSLHRSM
WCLEQKRQNMVLRBELTKINPTTVMSIYGKAAAKRLGDVISVSCQCPVNQATVTLRKSM

Figure 1(c)

236230 "495500T

HHV8PEP
RHEsrHADPEP
MURH68PEP
BOVINEH4PEP
ATELINEH3PEP
SAIMIRIPEP
EQH2PEP
EQH5PEP
ALCELPEP
EBVPEP

RTN---SKDVCYARPLVTFKFLNSSNLFTGQLGARNEIILTNNQVETCKDTCEHYFITRN
RTS---TPGMCYSRPPVTFRFLNSTTLFKGQLGPRNEIILTNDQVEACKETCEHYFIASN
RLQH---DKTTCYSRPRVTFKFINSTDPLTGQLGPRKEIILSNTNIECKDESEHYFIVGE
RTD---DPKVCYSRPLVTFKFVNSTATFRGQLGTRNEILLTNTHVETCRPTADHYFFVK
KTT---NNDVCYSRPPVTFKFVNSSQLFKGQLGARNEILLSSESLVENCHQNAEHFFAKN
KTE---NNDICYSRPPVTFKFVNSSQLFKGQLGARNEILLSSESLVENCHQNAETFFAKN
KVPG---KEDLCYTRPVVGFKFINGSSELFAGQLGPRNEIVLSTSQVEVCQHSCEHYFQAGN
RVPG---SKDLCYTRPVVGFKFINGSSELFVQQLGARNEILLSTNLVEVCQHSCEHYFQGGN
RVPGRDKTHECYSRPPVTFKFINDSHLYKGQLGVNNEILLTTTAVEICHENTEHYFQGGN
RVPG---SETMCYSRPLVSFSFINDTKTYEGQLGTDNEIFLTKKMTEVCQATSQYYFQSGN

HHV8PEP
RHEsrHADPEP
MURH68PEP
BOVINEH4PEP
ATELINEH3PEP
SAIMIRIPEP
EQH2PEP
EQH5PEP
ALCELPEP
EBVPEP

ETLVYKDYAYLRTINTTDTISLTNFIALNLSFIQNIIDFKAIELYSSAEKRCLASSVFDLET
VTYYYKDYVFKKINTSEISTLGTFIALNLSFIENIDFRVIELYSRAEKKLSGVSVDIET
YIYYKDYIFEEKLNLSIATLDTFIALNLSFIENIDFKTVELYSSTERKLASSVFDIES
MTHYFKDYKFKVKTMDTNISTLDTFLTLNLTFDIDNIDFKTVELYSETERKMAS-ALDLET
ETYHFKNYLHVETLPLTNISTLDTFLALNLTFIENIDFKAVELYSSGERKLAN-VFDLET
ETYHFKNYVHVETLPLNNISTLDTFLALNLTFIENIDFKAVELYSSGERKLAN-VFDLET
QMYKYKDYVYSTLNLTDIPLHTMITLNLSTVENIDFKVIELYSKTEKRLSN-VFDIET
HIYKYKDYVYSTMLNLTDPVTLHTMITLNLSTVENIDFQVIQLYSQEKKLSN-VFDIET
NMYFYKNYRHVKTMPVGDVATLDTFMVLNLTVENIDFQVIELYSREKRMST-AFDIET
EIHVYNDYHHFKTIELDGIATLQTFISLNTSLIENIDFASLELYSRDEQRASN-VFDLEG

HHV8PEP
RHEsrHADPEP
MURH68PEP
BOVINEH4PEP
ATELINEH3PEP
SAIMIRIPEP
EQH2PEP
EQH5PEP
ALCELPEP
EBVPEP

MFREYNYTHRLAGLREDLNTIDMNERFVRDLSEIVADLGGIGKTVNVASSVVTLCG
MFREYNYTQRLAGLREDLNTIDLNRDRLARDLSEIVADLGDVGRTVNVASSVITLFG
MFREYNYTYSLAGIKKDLNTIDYNDRDLVQDLSMDLGDIGRSVNVVSSVVTFFS
MFREYNYTQKLASLREDLNTIDLNRDRLVKDLSEMMADLGDIGKVVNTFSGIVTVFG
MFREYNYAQSIISGLRKDFDNSQRNNRDRIIQDFSEILADLGSIGKVIIVNIASSAFSLFG
MFREYNYAQSIISGLRKDFDNSQRNNRDRIIQDFSEILADLGSIGKVIIVNVASGAFSLFG
MFREYNYTQNLNGLRKDLDDSIDHGRDSFIQTLGDMQDLGTIGKVVNVASGVFSLFG
MFREYNYTQNLKGLRKDLDDSIDHGRDSFIQFLGDLVQDLVPVGDVIVNVASGVFSLFG
MFREYNYTQRTVGLRRDLTD-LATNRNQFVDAFGSLMDDLGVVGKTVLNAVSSVATLFS
IFREYNFQAQNIAGLRKDLDNAVSNRGNQFVDGLGELMDSLGSVGQSITNLVSTVGGFLS

HHV8PEP
RHEsrHADPEP
MURH68PEP
BOVINEH4PEP
ATELINEH3PEP
SAIMIRIPEP
EQH2PEP
EQH5PEP
ALCELPEP
EBVPEP

SLVTGFINFIKHPGLGMLMIIIVIAIILIIIFMLSRRTNTIAQAPVKMIYP---DVDRRA
SIVSGFINFIKSPFGGMLMILVIVAVVLIVFALNRRNTAIAQAPIRMIYP---DIDKMQ
SIVTGFIKFFTNPLGGIFILLIIGGIIFLVVVLNRRNSQFHDAPIKMLYPSVENYAARQA
SIVGGFVSFFTNPIGGVTIILLVIVVVFVIVSRRTNNMNEAPIKMIYP---NIDKAS
GIVTGILNFIKNPLGGMLTFLLVGAIILVILLVRRTNMNSQAPIRMIYP---DIEKSR
GIVTGILNFIKNPLGGMFTFLLAGVAILVILLVRRTNMNSQAPIRMIYP---DVEKSK
SIVSGVISFFKNPFGGMLLIVLIAGVVVVYLFMTRSRISIYAPIRMLYP---GVERAA
SIVSGVISFLKNPLGAILTIALIVGGIIVLYLFIITRSRTVYQAPIRMLYP---EVDRA
SIVSGIINFIKNPFGGMLLFLGLIAAVVITVILLNRKAKRFAQNPVQMIYP---DIKTIT
SLVSGFISPFKNPFGGMLLILVLVAGVVILVISLTRRTRQMSQPVQMLYP---GIDELA

HHV8PEP
RHEsrHADPEP
MURH68PEP
BOVINEH4PEP
ATELINEH3PEP
SAIMIRIPEP
EQH2PEP
EQH5PEP
ALCELPEP
EBVPEP

PP-----SGGAPTREEIKNILLGMHQLQQ---ERQKADDLKKSTPSVFQRTANGLR
P-----SGGKVDQEQIKNILAGMHQLQQ---EERRRLDEQORSAPSLFRASDGLK
PPPYSA---SPPAIDKEEIKRILLGMHQLVHQ---EEKEAQQLTNSGPTLWQKATGFLR
EQE-----NIQPLPGEEIKRILLGMHQLQQ---SEHGKSEEEASHKPGFLQLLGDGLQ
S-----SVTPTEPEVIKQILLGMHNMQQ---EYKKEEHKASQPSFLKRATDAFL
S-----TVTPMEPETIKQILLGMHNMQQ---EAYKKKEEQRAARPSIFRQAAETFL
QEP-----GAHPVSEDQIRNLMGMHGFQQRQRAEEEARREEVKGKRTLFEVIRDSAT
QQ-----NVQPIPEDQVRSILLAMHGFQQQQQQQQQQQQEHTQ-RRSIFDTIRESTS
SQREEL---QVDPISKHELDRIMLAMHDYHASK---QPESKQDEEQGSTTSGPADWLNKAK
QQHASGEGPGINPISKTELQAIMLALHEQNQ-----EQKRAAQRAAGPSVASRALQAAR

Figure 2

[illegible]

Figure 4

pGHV-gpB DNA.txt	-----AATCT	TCGTATCAGA	ATAAATAACA	25
pGHV1 DNA. (641-1300)	CGCCGCCGTC	CGGCTCCACG	GTGGTGCGGC	688
		T G C GA A C		
pGHV-gpB DNA.txt	TTTTGGAAGA	TTTGTCAAAG	GCATGGTGTC	75
pGHV1 DNA. (641-1300)	GCCCCGAGTA	CTCG-CAGGG	GCGCAACTTC	737
	GA A T G CA G GC TC	G G A T G TGCT		
pGHV-gpB DNA.txt	CTGGTGTGGA	ATGAGCTCAG	CAAGATTAAT	125
pGHV1 DNA. (641-1300)	CT----T-CA	AGGAGAACAT	C--G-CC--C	776
	CT T A A GAG CA C G	C CACAAG	TCA G C	
pGHV-gpB DNA.txt	GATTTACAAT	-AGACCCGTA	TCAGC-CAAA	172
pGHV1 DNA. (641-1300)	CATCTACTAC	AAGAAGCTCA	TCGTACAGAC	826
	AT TAC A AGA C A TC C C A	G T G G CA T		
pGHV-gpB DNA.txt	CAGTCTCTAA	C-TGTATTG-	-TGGTAGACC	219
pGHV1 DNA. (641-1300)	ACGCGGCCAT	CACGAACCGC	TTCACAGACC	876
	G C A C G A G T AGACC	GT C C T CA		
pGHV-gpB DNA.txt	AAAAGTCTCA	GGCTTCTCAG	TGCATCGGAT	269
pGHV1 DNA. (641-1300)	GAGA-TCACG	GACGTGATCG	ACCGCCG--C	922
	A A TC C C T G C CG	G AAGTG C TCTC A A		
pGHV-gpB DNA.txt	TCCAGTGACA	T--TTAA-GT	TTATGA-ATG	314
pGHV1 DNA. (641-1300)	CCGAGT-ACG	TGCGCAACAA	CCACAAGGTG	971
	C AGT AC T AA A A TG	AC G T C AG		
pGHV-gpB DNA.txt	GCAACTAG--	GAGTCAATAA	TGAGATTCT-	354
pGHV1 DNA. (641-1300)	GAACCCCGTC	GAGGTGGACC	TGCGCCCTC	1021
	G A C GAG TG G CT	CT AAC C C		
pGHV-gpB DNA.txt	TAC-C--TTG	AAACA-TGTC	-AGGAAA---	395
pGHV1 DNA. (641-1300)	CCCGCGGCTG	GCACACCACC	AACGACACCT	1071
	C C TG ACA C A GA A	ACAC AG C C		
pGHV-gpB DNA.txt	GGCAAAGACA	GACATGTACA	TTTACAAAAA	439
pGHV1 DNA. (641-1300)	GGCTTCTAC-	CACACGGGCA	CCTCCGTCAA	1120
	GGC AC ACA G CA T C AA	CT AT GAG A TG		
pGHV-gpB DNA.txt	AGAC-----	--TGTGCCTT	TA-----TCT	476
pGHV1 DNA. (641-1300)	AGGCGCGCTC	CGTGTACCCC	TACGACTCCT	1170
	AG C TGT CC TA CT	TCG C CAC G AC		
pGHV-gpB DNA.txt	ATT---TATA	GCCCTTAATT	TTAC--ACTA	521
pGHV1 DNA. (641-1300)	ATTGTGTACA	TGTCCCCCTT	CTACGGCCTG	1220
	ATT TA A C TT TAC T	GAG G AC A		
pGHV-gpB DNA.txt	AGTCATTGAA	CTTTATACCA	GGG----ACG	564
pGHV1 DNA. (641-1300)	GCACATCG-G	CTACGCGCCC	GGGCGCTTCC	1269
	CAT G CT CC GGG C AG	G G G A TA A		
pGHV-gpB DNA.txt	GTCTTTGACA	TTGAAACAAT	G-----	585
pGHV1 DNA. (641-1300)	CCCATCGAC-	CTGGACTCGC	GCCTCCGCGC	1300
	C T GAC TG A G			

Figure 5

pGHV-gpB prot	-----N LRI-----	4
PGHV1Prot. (491-850)	PAAPAAARRA RRSPGPAGTP EPPAVNGTGH LRITGSAEF ARLQFTYDHI LRI	540
pGHV-gpB prot	--RINNILED LSKAWCREQH RAALVWNELS KINPTSVMSM IYNRPVSAKR	52
PGHV1Prot. (491-850)	QAHVNDMLGR IAAAWCELQN KDRTLWSEMS RLNPASAVATA ALGQRVASARM N L AWC Q W E S NP V VSA	590
pGHV-gpB prot	IGDVISVSNC IVVDQTSVSL HKSLRLLSAS DEKCFSRPPV TFKFMNDSTI	102
PGHV1Prot. (491-850)	LGDVMAISRC VEV-RGGVYV QNSMR-VPGE RGTCYSRPLV TFE-HNGTGV GDV S C V V S R C SRP V TF N	637
pGHV-gpB prot	YKQQLGVNNE ILLTTTylet COENTeYYFQ AKTDMYIYKN YEHLKTVPLS	152
PGHV1Prot. (491-850)	IEGQLGDDNE LLISRDLIEP CTGNHRRYFK LGSGYVYYED YNYVRMVEVP GQLG NE L E C N YF Y Y V	687
pGHV-gpB prot	SITTLDTFIA LNFTLLENVD FKVIELYTRD E----- --KR----	185
PGHV1Prot. (491-850)	--ETISTRVT LNLTLLEDRE FLPLEVYTRE ELADTGLLDY SEIQRRNQLH T LN TLLE F E YTR E R	735
pGHV-gpB prot	-----	185
PGHV1Prot. (491-850)	ALKFYDIDRV VKVDHNVVLL RGIANFFQGL GDVGAAVGKV VLGATGAVIS	785
pGHV-gpB prot	-----LS NVF-----	190
PGHV1Prot. (491-850)	AVGGMVSFLS NPPGALAIGL LVLAGLVAAF LAYRHISRLR RNPMKALYPV LS N F	835
pGHV-gpB prot	-----DI E--TM	195
PGHV1Prot. (491-850)	TTKTLKEDGV DEGDV	850

[illegible]

Figure 7

pGHV-gpB prot	NLRIRINNIL EDLSKAWCRE QHRAALVWNE LSKINPTSVM SMIYNRPVSA	50
pGHV2 prot.txt	S--IMIANNL -----C-- --YSTLI--- LNDEDVTG-- -----IDE	25
	I I N L C L L T	
pGHV-gpB prot	KRIGDVISVS NCIVVDQTSV SLHKSLRLLS ASDEKCFSRP PVTFKFMNDS	100
pGHV2 prot.txt	K---DILTVH ---VNQNTV-----YRFVRSS	45
	K D V V V F S	
pGHV-gpB prot	---TIYKGQL GV-NNBILLT TTYLSTCOEN TEYFFQAKTD MYI---YKN-	142
pGHV2 prot.txt	VRESILGTLL SRWLRKRKEV KARMKRCEDP MLALILDKQQ LALKVTCNAF	95
	I L C K	
pGHV-gpB prot	YEHLKTVP-- LSSITTLDTF IALNFTLL-E NVDFKVIELY TRD---EK-R	185
pGHV2 prot.txt	YGFTGAVHGL LPCLPLAASI TSIGRDMLRQ TSDFINNVLS SREYVSEKFS	145
	Y V L L DF L R EK	
pGHV-gpB prot	LSNV-F--DI ETM-	195
pGHV2 prot.txt	LSDGDFQGDF SPEC	159
	LS F D	

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Figure 8

pGHV-gpB DNA	AATCTTCGTA	TCAGAATAAA	TAACATTTTG	GAAGATTGTG	CAAAGGCATG	50
AF118399 DNA.txt	-----	-----	-----	-----	-----	
pGHV-gpB DNA	GTGTCGTGAG	CAGCATAGAG	CTGCTCTGGT	GTGGAATGAG	CTCAGCAAGA	100
AF118399 DNA.txt	-----	-----	-----	-----	-----	
pGHV-gpB DNA	TTAATCCCAC	AAGCGTCATG	AGCATGATTT	ACAATAGACC	CGTATCAGCC	150
AF118399 DNA.txt	-----	-----	-----	-----	-----	
pGHV-gpB DNA	AAAAGAATAG	GAGATGTCAT	TTCAGTCTCT	AACTGTATTG	TGGTAGACCA	200
AF118399 DNA.txt	-----	-----	-----	-----	-----	
pGHV-gpB DNA	AACCAGTGTC	TCATTACATA	AAAGTCTCAG	GCTTCTCAGT	GCATCGGATG	250
AF118399 DNA.txt	-----	-----	-----	-----	-----	
pGHV-gpB DNA	AAAAGTGCTT	CTCTAGACCT	CCAGTGACAT	TTAAGTTTAT	GAATGACAGT	300
AF118399 DNA.txt	-----	-----	-----	-----TAAT	CTATGTCACT	14
				T AT	ATG CA T	
pGHV-gpB DNA	ACTATTTACA	AAGGGCAACT	AGGA-GTCAA	TAATGAGATT	CTCTTAACCA	349
AF118399 DNA.txt	-CTACCC-TA	ATCCATCATG	AAGACCTGCA	TAAATATCCT	CAATTAAAGG	62
	CTA A A	A A	A GA T A	TAA A T A	TTAA	
pGHV-gpB DNA	CAACATACCT	TGAAACATGT	CAGGAAAACA	CTGAGTATTA	CTTTCAGGCA	399
AF118399 DNA.txt	AGGAGGATTA	TGAAACAT--	-----	-----	-TTT-----	83
	A	TGAAACAT			TTT	
pGHV-gpB DNA	AAGACAGACA	TGTACATTTA	CAAAAACTAT	GAGCATTGTA	AGACTGTGCC	449
AF118399 DNA.txt	-----	TG---ATT--	-----	-AG---TT--	---CTG----	95
		TG ATT		AG TT	CTG	
pGHV-gpB DNA	TTTATCTTCG	ATCACCACAC	TAGATACATT	TATAGCCCTT	AATTTTACAC	499
AF118399 DNA.txt	-----	-----	-----	----GTCC--	-----	99
				GTCC		
pGHV-gpB DNA	TATTGGAGAA	TGTTGACTTT	-----AAAG	TCAT-T--GA	A---CTT---	534
AF118399 DNA.txt	-----	TGTTCACTTT	GTAAAAAAAC	ACATATCAGA	ATCTCTTCTG	139
		TGTT ACTTT	AAA	CAT T GA A	CTT	
pGHV-gpB DNA	--TA-----	-TAC--CA--	G--GG--ACG	AGA-----	--AG--AGG-	555
AF118399 DNA.txt	TCTAACCTGC	TTACAACATG	GCTGGCTAAG	AGAAAAATGA	TCAGAAAGGA	189
	TA	TAC CA	G GG A G	AGA	AG AGG	
pGHV-gpB DNA	CTTAGTA--A	TGT-CT--TT	GACA-TTGA-	AACAATG---	-----	585
AF118399 DNA.txt	ATTAGCAGCA	TGTGCTGACC	CAAAGCTCAG	GACAAT-TTT	AGATAAACAG	238
	TTAG A A	TGT CT	A A T A	ACAAT		
pGHV-gpB DNA	-----	-----	-----	-----	-----	585
AF118399 DNA.txt	CAGCTTGCAA	TTAAGGTGAC	ATGCAATGCT	GTGTATGGGT	TCACTGGTGT	288
pGHV-gpB DNA	-----	-----	-----	-----	-----	585
AF118399 DNA.txt	TGCATCTGGT	ATGCTGCCCT	GTCTCAAGAT	TGCAGAGACC	ATAACTATGC	338
pGHV-gpB DNA	-----	-----	-----	-----	-----	585
AF118399 DNA.txt	AAGGAAGGGC	CATGTTGGAA	AAGACAAAAG	TATTTGTAGA	GAATTTAAGT	388
pGHV-gpB DNA	-----	-----	-----	-----	-----	585
AF118399 DNA.txt	CATGAGGATC	TCCATTCCAT	CTGTAAGGTT	GGCTTTATGC	CTCAGTCACC	438
pGHV-gpB DNA	-----	-----	-----	585		
AF118399 DNA.txt	AAACAGCATT	GATAAACCTT	TCAAGGTG	466		

Figure 10

Query: 1970 aagtcattgaactttataaccagggacgagaagaggcttagtaatgtctttgacattgaaa 2029
||||| ||| ||||| || | ||| ||| ||||| ||| ||| ||| ||||| ||| |||
Sbjct: 18669 aagtaatagaactatactctagagaagagaagaggatgagcactgcatttgatatagaga 18728
Query: 2030 caatgttttagggaatataactactatgctcagaggggtcagtgccctcagaaaggatttgc 2089
||||| ||| ||||| ||||| ||| ||||| ||||| ||||| ||| ||| ||| |||
Sbjct: 18729 ccatgttttagagaatacaactactacacacagaggggtcactggcctgaggaggacttga 18788
Query: 2090 tggatctaagcaccaatagaaatcaatttgggatgcatttggtagtcttatggatgatt 2149
|| ||| || ||| ||||| ||||| ||||| ||||| ||| ||| ||| |||
Sbjct: 18789 cagacctagctacaaacagaaatcaatttgtagatgcctttggcagcctcatggacgact 18848
Query: 2150 tgggtgctggttgggcagacagttgtaaatgctgtaagtgggtgtggctacgctgttttagct 2209
||||| ||| ||| ||| ||| ||| ||||| ||| ||||| ||| ||||| ||| |||
Sbjct: 18849 tgggggtcgtggggaaaacggtgttgatgctgtgagcagtggtggccacactcttcagct 18908
Query: 2210 caattgtaacaggattttattaatttcattaaaaacccatttgggtggaatgtt 2261
|| ||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 18909 ctatagtctcagggatcatcaatttcattaaaaacccctttgggggaatgtt 18960

Score = 91.1 bits (47), Expect = 7e-16
Identities = 117/152 (76%), Positives = 117/152 (76%)

Query: 1498 tgggtgctgtagcagcatagagctgctctggtgtggaatgagctcagcaagattaatccc 1557
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 18194 tgggtgccgtgagcagcaccgagcctctctcatgtggaacgagctaagcaaaatcaaccct 18253
Query: 1558 acaagcgtcatgagcatgatttacaatagaccggtatcagccaaaagaataggagatgtc 1617
|| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 18254 accagtgtgatgagctctatatacgggcgccagtatctgccaaaagaattggagatgtg 18313
Query: 1618 atttcagtcctctaactgtattgtggttagacca 1649
|| ||| ||||| ||||| ||||| ||||| |||||
Sbjct: 18314 atatctgtctctcactgtgtggtggttagacca 18345

Figure 11(a)

gi|2337975 (AF005370) glycoprotein B [Alcelaphine herpesvirus 1]
Length = 854

Score = 953 bits (2437), Expect = 0.0

Identities = 463/804 (57%), Positives = 589/804 (72%), Gaps = 26/804 (3%)

Query: 74 KNIYGSPSTFPYRVCSASGVGDVFRFQTDHVCPCDASDMVHSEGILLIYKQNIIPFMFRVR 133
K I+ PS FP+RVCSAS +GD+FRFQT H CP+ D H+EGILLI+K+NI+P++F+VR
Sbjct: 55 KGIHSDPSAFPFRVCSASNIGDIFRFQTSHPSCNTKDKHEGILLIFKENIVPYVFKVR 114

Query: 134 KYRKVTTSTVYNGIYSDSITNQHTFYKSIEPWETEKMDTIYQCFNSLRLNTGGNLLTYV 193
KYRK+VTTST+YNGIY+D++TNQH F KS+ +ET +MDTIYQC+NSL + GGNLL Y
Sbjct: 115 KYRKIVTTSTIYNGIYADAVTNQHVFSKSVPIYETRRMDTIYQCYNSLDVTVGNNLLVYT 174

Query: 194 DRDDINMTVFLQPVDGVTDPVKRYGSQPELYLEPGWFGWSYRRRTTVNCELMDMFARSNP 253
D D NMTV LQPVDG++ V+RY SQPE++ EPGW G YRRRTTVNCE+ + AR+ P
Sbjct: 175 DNDGSNMTVDLQPVDGLSNSVRRYHSQPEIHAEPGWLLGGYRRRTTVNCEVTETDARAVP 234

Query: 254 PFDFEVTATGDTVEMSPFWSGEDDHENKMHEKPWFVSVINNYKVVDYQNRGTVPGLKTRI 313
PF +F+T GDT+EMSPFWS + E ++V +Y+VVDY+ RGT P G TRI
Sbjct: 235 PFRYFITNIGDTIEMSPFWSKAWNETEFSGEPDRTLTVAKDYRVVDYKFRGTQPPQHTRI 294

Query: 314 FLDREEYTLSEWEHLKNSYCPLTLWKAFYNGIQTEHSGSYHFVANDITASFTTSKEDMK 373
F+D+EEYTLSEW + +N+SYC WK+F N I+TEH S HFVANDITASF T +
Sbjct: 295 FVDKEEYTLSEWQQFRNISYCRWAHWKSFDAIKTEHGKSLHFVANDITASFYTPNTQTR 354

Query: 374 EFNTTYHCLNXXXXXXXXXXXXXXXXXVNSTHSHYKGLKYFKTDGGLYLWVQPLIQNRLLDAKN 433
E + CLN VN THS G +Y+ T+GGL LVWQPL+Q +LLDAK
Sbjct: 355 EVLGKHVCLNNTIESELKSRLAKVNDTHSPNGTAQYYLTNGGLLLWVQPLVQQLLDAKG 414

Query: 434 KLN-----NETYSRRSRRQAESTTDPMMEMTGNGAGGEYSSENSITVAQVQYAYDN 484
L+ T + RSRRQ S + +G Y++E++I + Q+Q+AYD
Sbjct: 415 LLDVAVKKQNTTTTTTTTTTSRRRQRRSVS-----SGIDDVYTAESTILLTQIQFAYDT 466

Query: 485 LRIRINNILEDLKAWCREQHRAALVWNELSKINPTSVMSMIYNRPVSAKRIGDVISVSN 544
LR +INN+LE+LS+AWCREQHRA+L+WNELSKINPTSVMS IY RPSAKRIGDVISVS+
Sbjct: 467 LRAQINNVLLELSRAWCREQHRASLMWNELSKINPTSVMSIYGRPVSAKRIGDVISVSH 526

Query: 545 CIVVDQTSVSLHKSRLRLLSA-SDEKCFSRPPVTFKFMNDSTIYKQGLGVNNEILLTTTYL 603
C+VVDQ SVSLH+S+R+ +C+SRPPVTFKF+NDS +YKQGLGVNNEILLTTT +
Sbjct: 527 CVVVDQDSVSLHRSRMRVPGRDKTHECYSRPPVTFKFINDSHLYKQGLGVNNEILLTTTAV 586

Query: 604 ETCQENTEEYFQAKTDMYIYKNYHLKTVPLSSITTLDTFIALNFTLLENVDFKVIELYT 663
E C ENTE+YFQ +MY YKNY H+KT+P+ + TLDTF+ LN TL+EN+DF+VIELY+
Sbjct: 587 EICHENTEYFQGGNNMYFYKNYRHVKTMPVGDVATLDTFMVLNLTLENIDFQVIELYS 646

Query: 664 RDEKRLSNVFDIETMFREYNYYAQRVSGLRKDLLDLSTNRNQFVDAFGSLMDDLGVGQT 723
R+EKR+S FDIETMFREYNYY QRV+GLR+DL DL+TNRNQFVDAFGSLMDDLGVG+T
Sbjct: 647 REEKRMSAFDIETMFREYNYYTQRVTLRRDLTDLATNRNQFVDAFGSLMDDLGVVGKT 706

Figure 11(b)

Query: 724 VVNAVSGVATLFSSIVTGFINKNPFGGMLMIIVVIGVLFAYFLTKKTKIYETAPIKM 783
V+NAVS VATLFSSIV+G INFIKNPFGGML+ ++ V+ + L +K K + P++M
Sbjct: 707 VLNAVSSVATLFSSIVSGIINFIKNPFGGMLLFGLIAAVVITVILLNRKAKRFAQNPVQM 766

Query: 784 IYPEIDKLKEREKSEIAPISEEEELERIVLAMHIHQONSHMETK-----TRKDPKDSI 836
IYP+I + + + ++ PIS+ EL+RI+LAMH + + E+K T P D
Sbjct: 767 IYPDIKTITSQREELQVDPISKHELDRIMLAMHDYHASKQPESKQDEEQGSTTSGPAD-W 825

Query: 837 LTRAQNMLRKRSYGYSNLKNAESVE 860
L +A+N+LR+R+GY LK +S E
Sbjct: 826 LNKAKNVLRRRAGYKPLKRTDSFE 849

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